

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:35:35 ; Search time 28 Seconds
(without alignments)
88.306 Million cell updates/sec.

Title: US-09-551-151A-43

Perfect score: 64

Sequence: 1 SPOGIAGQRNFM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4583

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	42.2	17	6	046473
2	25	39.1	13	4	P82276
3	23	35.9	8	5	P83316
4	23	35.9	10	5	P83280
5	22	34.4	10	2	09X3M2
6	22	34.4	11	2	09S623
7	22	34.4	13	2	09X3E1
8	22	34.4	13	2	09X3J6
9	22	34.4	13	4	08WY56
10	22	34.4	15	10	09S8V7
11	22	34.4	16	5	09TWK0
12	22	34.4	17	2	09X3I3
13	22	34.4	18	2	09X3H7
14	21	32.8	9	5	P83279
15	21	32.8	15	8	P82135
16	21	32.8	16	5	09TWK1

17	21	32.8	17	4	09UC72	09UC72 homo sapien
18	20	31.2	8	2	09X3K1	09X3K1 prochloroco
19	20	31.2	11	2	09A1Z8	09A1Z8 carsonella
20	20	31.2	12	12	086570	086570 hepatitis d
21	20	31.2	13	4	09U773	09U773 homo sapien
22	20	31.2	15	2	09R586	09R586 serratia ma
23	20	31.2	15	12	09PXC5	09PXC5 tobacco etc
24	20	31.2	17	4	09UC89	09UC89 homo sapien
25	20	31.2	17	10	P82947	P82947 glycine max
26	20	31.2	18	2	09R4F3	09R4F3 escherichia
27	20	31.2	18	4	09UE43	09UE43 homo sapien
28	20	31.2	18	4	09UE38	09UE38 homo sapien
29	20	31.2	18	5	09TWV6	09TWV6 aplysia cal
30	19.5	30.5	14	2	09R517	09R517 escherichia
31	19	29.7	9	4	014715	014715 homo sapien
32	19	29.7	10	11	09QV66	09QV66 mus sp. pro
33	19	29.7	14	2	P83077	P83077 bacillus ce
34	19	29.7	15	2	P83069	P83069 bacillus ce
35	19	29.7	15	4	09UC90	09UC90 homo sapien
36	19	29.7	16	4	09UC88	09UC88 homo sapien
37	19	29.7	16	11	09QUW5	09QUW5 rattus sp.
38	19	29.7	18	4	09POM3	09POM3 homo sapien
39	19	29.7	18	5	09TWM9	09TWM9 tetrahymena
40	18.5	28.9	18	4	08WYH0	08WYH0 homo sapien
41	18	28.1	10	2	09R7J8	09R7J8 helicobacte
42	18	28.1	10	13	09QY93	09QY93 gallus gall
43	18	28.1	11	2	047567	047567 escherichia
44	18	28.1	11	11	08R2J7	08R2J7 mesocricetu
45	18	28.1	12	4	09UMQ9	09UMQ9 homo sapien

ALIGNMENTS

RESULT 1

ID 046473 PRELIMINARY; PRT; 17 AA.
AC 046473;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Lactase dehydrogenase A (Fragment).
GN LDHA.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DOMESTICUS;
RX MEDLINE=97141918; PubMed=8988168;
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
O'Brien S.J.;
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of
RT mammalian genomes";
RL Nat. Genet. 15:47-56(1997).
DR EMBL; AF012095; AAC00072.2;
FT NON_TER 1 17
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 2018 MW; E47943B2E187C1FC CRC64;

Query Match 42.2%; Score 27; DB 6; Length 17;
Best Local Similarity 83.3%; Pred. No. 2,4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GQRNFM 12

Db 3 GQRNFM 8

RESULT 2

P82276 PRELIMINARY; PRT; 13 AA.

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AC P82276;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Tubulin-associated peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Rosbacher J., Gartner W., Kallinger H., Wagner L.,
RT "Haptoglobin mediated changes in cellular immune response."
RL Submitted (JAN-2000) to the SWISS-PROT data bank.
CC -1- TISSUE SPECIFICITY: LEUKOCYTES AND HEPATOCYTES.
KW Microtubules.
FT NON_TER 1 1
FT TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; 4FD05B1E478D62C7 CRC64;

Query Match 39.18; Score 25; DB 4; Length 13;
Best Local Similarity 57.18; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 G1AGORN 10
DB 5 G1VGOEN 11

RESULT 3
P83316 PRELIMINARY; PRT; 8 AA.
AC P83316;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE FMRamide-like neuropeptide Flrp (GDRNFLRP-amide).
OS Pennaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Pennaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Pennaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

Query Match 35.98; Score 23; DB 5; Length 8;
Best Local Similarity 80.08; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GORNF 11
DB 1 GDRNF 5

RESULT 4
P83280 PRELIMINARY; PRT; 10 AA.
AC P83280;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

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DE FMRamide-like neuropeptide Flrp7 (GYDRNFLRP-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-EYESTALK;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Sarathkum W., Longyant S., Panchan N.,
RT "Three more novel FMRamide-like neuropeptide sequences from the
eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;

Query Match 35.98; Score 23; DB 5; Length 10;
Best Local Similarity 80.08; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GORNF 11
DB 3 GDRNF 7

RESULT 5
09X3M2 PRELIMINARY; PRT; 10 AA.
ID 09X3M2;
AC 09X3M2;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE Cytochrome b (Fragment).
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070219; AAD33269.1;
FT NON_TER 1 1
FT SEQUENCE 10 AA; 1076 MW; 75CA5CH05866D324 CRC64;

Query Match 34.48; Score 22; DB 2; Length 10;
Best Local Similarity 80.08; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 G1AG 7
DB 5 G1SIS 9

RESULT 6
09S623 PRELIMINARY; PRT; 11 AA.
ID 09S623;
AC 09S623;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Cytochrome b (Fragment).
GN PRTB.
OS Prochlorococcus sp.

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OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
  sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070168; AAD23221.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1153 MW; 5F551A5CB05866D3 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OG1AG 7
    |||:|
    5 OG1SG 9

RESULT 7
OQX3E1 PRELIMINARY; PRT; 13 AA.
AC OQX3E1:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
  sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070141; AAD20755.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1434 MW; 57EBE8029A8666D3 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OG1AG 7
    |||:|
    7 OG1SG 11

RESULT 8
OQX3J6 PRELIMINARY; PRT; 13 AA.
AC OQX3J6:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
  sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).

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DR EMBL; AF070189; AAD23225.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1473 MW; 57FA9A029A8666D3 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OG1AG 7
    |||:|
    7 OG1SG 11

RESULT 9
OQWY56 PRELIMINARY; PRT; 13 AA.
AC OQWY56:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Epithelial sodium channel beta-3 subunit (Fragment).
GN SCN1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;
RT "Genomic organization of the 5' end of human beta ENAC and preliminary
  characterization of its promoter.";
RL Am. J. Physiol. Renal Physiol. 0:0-0(2002).
DR EMBL; AF260228; AAL48197.1; -.
KW Ionic channel.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;

Query Match 34.4%; Score 22; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 GIACGRNF 11
    | | : | |
    5 GNLGDKNF 12

RESULT 10
OQ58V7 PRELIMINARY; PRT; 15 AA.
AC OQ58V7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE High-molecular-weight glutenin subunit (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE.
RX MEDLINE=93003354; PubMed=1390908;
RA Tao H.P., Adalstein A.E., Kasarda D.D.;
RT "Intermolecular disulfide bonds link specific high-molecular-weight
  glutenin subunits in wheat endosperm.";
RL Biochim. Biophys. Acta 1159:13-21(1992).
SQ SEQUENCE 15 AA; 1559 MW; CD1A6F573C945AFD CRC64;

Query Match 34.4%; Score 22; DB 10; Length 15;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PG1AG 7

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Db 4 PGXG 9

RESULT 11

09TWKO PRELIMINARY; PRT; 16 AA.
 AC 09TWKO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
 DE Proximal collagen (Fragment).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 NCBI_TaxID=6550;
 RN NCBI_TaxID=6550;
 RP SEQUENCE.
 RX MEDLINE=95230211; PubMed=7714453;
 RA Qin X., Waite J.H.;
 RT "Exotic collagen gradients in the byssus of the mussel Mytilus
 edulis.";
 RL J. Exp. Biol. 198;633-644(1995).
 SO SEQUENCE 16 AA; 1347 MM; B57F18783A18783C CRC64;

Query Match 34.4%; Score 22; DB 5; Length 16;
 Best Local Similarity 66.7%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PGXG 7
 Db 5 PGXG 10

RESULT 12

09X313 PRELIMINARY; PRT; 17 AA.
 AC 09X313;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE Cytochrome b (Fragment).
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 NCBI_TaxID=1220;
 RN NCBI_TaxID=1220;
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanogr. 43;1615-1630(1998).
 DR EMBL; AF070176; AAD20791.1;
 FT NON_TER 1
 SO SEQUENCE 17 AA; 1953 MM; 630843039ADD51B4 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OGIG 7
 Db 11 OGIG 15

RESULT 13

09X3H7 PRELIMINARY; PRT; 18 AA.
 AC 09X3H7;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 SO SEQUENCE 17 AA; 1953 MM; 630843039ADD51B4 CRC64;

DE Cytochrome b (Fragment).
 GN PEB.

OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 NCBI_TaxID=1220;
 RN NCBI_TaxID=1220;
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanogr. 43;1615-1630(1998).
 DR EMBL; AF070170; AAD20782.1;
 FT NON_TER 1
 SO SEQUENCE 18 AA; 2117 MM; 09842D229ADD51A5 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OGIG 7
 Db 12 OGIG 16

RESULT 14

P83279 PRELIMINARY; PRT; 9 AA.
 AC P83279;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE FMRFamide-like neuropeptide FLP6 (DGGRNFRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 NCBI_TaxID=79674;
 RN NCBI_TaxID=79674;
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-EYE-STALK.
 RA MEDLINE=21107394; PubMed=11179812;
 RA Sithigorngul P., Sarathkum W., Longyant S., Panchan N.,
 RA Sithigorngul W., Petsom A.;
 RT "Three more novel FMRFamide-like neuropeptide sequences from the
 eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Peptides 22;191-197(2001).
 CC -1- MASS SPECTROMETRY: MW=1080.7; METHOD-MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 9
 FT MOD_RES 9
 SO SEQUENCE 9 AA; 1081 MM; 26800729C4540878 CRC64;

Query Match 32.8%; Score 21; DB 5; Length 9;
 Best Local Similarity 80.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GORNF 11
 Db 2 GORNF 6

RESULT 15

P82135 PRELIMINARY; PRT; 15 AA.
 AC P82135;
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
 DE Chloroplast 30S ribosomal protein S18 alpha (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC STRAIN-CV. ALVARO; TISSUE-LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465(2000).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MISCELLANEOUS: S18 ALPHA AND BETA FORMS DIFFER IN PI. S18 BETA
 CC FORM IS THE LEAST BASIC FORM.
 CC -1- MASS SPECTROMETRY: MW=12093; METHOD-MALDI.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.
 CC -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001648; Ribosomal_S18.
 DR Pfam: PF01084; Ribosomal_S18; PARTIAL.
 DR PROSITE: PS00057; RIBOSOMAL_S18; PARTIAL.
 KW Ribosomal protein; Chloroplast.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1910 MW; C29396F592403860 CRC64;

Query Match 32.8%; Score 21; DB 8; Length 15;
 Best Local Similarity 57.1%; Pred. No. 3,1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 IAGORNF 11
 I :|||
 Db 9 IKRRNF 15

Search completed: May 16, 2003, 10:38:03
 Job time : 29 secs

